

TELEX: 200797 NIXN UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 525 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..522
 OTHER INFORMATION: /product= "HUMAN GRANULOCYTE COLONY STIMULATING FACTOR"
 US-08-434-411-1

Query Match 93.3%; Score 486.8; DB 1; Length 525;
 Best Local Similarity 98.6%; Pred. No. 2..3e-109;
 Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

25 CTACACAGAGCTCTTAAAGCTTAGACAAAGTGGAAAGATCCAGGGATGGC 84
 Db 25 CTGCCAGAGCTCTGCTAGTGTAGCAAGTGGAAAGATCCAGGGATGGC 84
 Qy 85 GCAGGGCTCCAGGAAGAAAGCTGTGGCCACCTAACAGCTGTGGCACCCGAGGGCAGGGTGTG 144
 Db 85 GCAGGGCTCCAGGAAGAAAGCTGTGGCCACCTAACAGCTGTGGCACCCGAGGGCAGGGTGTG 144
 Qy 145 CTGCTGGGACACTCTGGGATCCCTGGCTGAGGAGCTGCCAGGCC 204
 Db 145 CTGCTGGGACACTCTGGGATCCCTGGCTGAGGAGCTGCCAGGCC 204
 Qy 205 CTGAGCTGGAGGGCTGCTGTGGCAACTCCATAGGGCCCTTTCCTCTAACAGGGCTC 264
 Db 205 CTGAGCTGGAGGGCTGCTGTGGCAACTCCATAGGGCCCTTTCCTCTAACAGGGCTC 264
 Qy 265 CTGAGGCCCTGGAGGGATCTCCCGAGTGTGTCACCTGGACACCTGGAGCTG 324
 Db 265 CTGAGGCCCTGGAGGGATCTCCCGAGTGTGTCACCTGGACACCTGGAGCTG 324
 Qy 325 GACGTCGCCGACTTGGCCACCATCGGCCAGAGAAACTGGGAATGGCCCT 384
 Db 325 GACGTCGCCGACTTGGCCACCATCGGCCAGAGAAACTGGGAATGGCCCT 384
 Qy 385 GCCCCGAGCCACCCAGGGTGCATGGGGCTTCGCTCTGGCTTCAGGGCCGGCA 444
 Db 385 GCCCCGAGCCACCCAGGGTGCATGGGGCTTCGCTCTGGCTTCAGGGCCGGCA 444
 Qy 445 GGAGGGTCCAGTGTGGCTCCATCTGGAGGCTTCCTGGAGGTGTGTAACGGCTCTTA 504
 Db 445 GGAGGGTCCAGTGTGGCTCCATCTGGAGGCTTCCTGGAGGTGTGTAACGGCTCTTA 504
 Qy 505 CGCCACCTGGCCAGCCC 522
 Db 505 CGCCACCTGGCCAGCCC 522

RESULT 2
 US-08-434-402-1
 Sequence 1, Application US/08434402
 Patent No. 5714581
 GENERAL INFORMATION:
 APPLICANT: KOGA, TETSURO
 APPLICANT: MIYAJI, HIROMASA
 APPLICANT: SATO, MORYUKI
 APPLICANT: OKABE, MASAMI
 APPLICANT: MORIZONO, MAKORO
 APPLICANT: ITOH, SEIGA
 APPLICANT: YAMASAKI, MOTOO
 APPLICANT: YOKO, YOSHIIHARU
 APPLICANT: YAMAGUCHI, KAZUO
 APPLICANT: YOSHIDA, HAJIME
 APPLICANT: YOSHINORI, KOMATSU

TITLE OF INVENTION: NOVEL POLYPEPTIDES
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434,402
 FILING DATE: 03-MAY-1995
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 306799/86
 FILING DATE: 23-DEC-1986
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 51357/88
 FILING DATE: 04-MAR-1988
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 80088/88
 FILING DATE: 31-MAR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAWFORD, ARTHUR
 REGISTRATION NUMBER: 25327
 REFERENCE/DOCKET NUMBER: 249-7-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 TELEX: 200797 NIXN UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 525 base pairs
 NAME/KEY: CDS
 LOCATION: 1..522
 OTHER INFORMATION: /product= "HUMAN GRANULOCYTE COLONY STIMULATING FACTOR"
 US-08-434-402-1

Query Match 93.3%; Score 486.8; DB 1; Length 525;
 Best Local Similarity 98.6%; Pred. No. 2..3e-109;
 Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

25 CTACACAGAGCTCCCTTAAAGCTTAGACAAAGTGGAAAGATCCAGGGATGGC 84
 Db 25 CTGCCAGAGCTCCCTTAAAGCTTAGACAAAGTGGAAAGATCCAGGGATGGC 84
 Qy 25 CTGCTGGGACACTCTGGGATCCCTGGCTGAGGAGCTGCCAGGCC 204
 Db 25 CTGCTGGGACACTCTGGGATCCCTGGCTGAGGAGCTGCCAGGCC 204
 Qy 205 CTGAGCTGGAGGGCTGCTGTGGCAACTCCATAGGGCCCTTTCCTCTAACAGGGCTC 264
 Db 205 CTGAGCTGGAGGGCTGCTGTGGCAACTCCATAGGGCCCTTTCCTCTAACAGGGCTC 264
 Qy 265 CTGAGGCCCTGGAGGGATCTCCCGAGTGTGTCACCTGGACACCTGGAGCTG 324
 Db 265 CTGAGGCCCTGGAGGGATCTCCCGAGTGTGTCACCTGGACACCTGGAGCTG 324
 Qy 325 GACGTCGCCGACTTGGCCACCATCGGCCAGAGAAACTGGGAATGGCCCT 384
 Db 325 GACGTCGCCGACTTGGCCACCATCGGCCAGAGAAACTGGGAATGGCCCT 384
 Qy 385 GCCCCGAGCCACCCAGGGTGCATGGGGCTTCGCTCTGGCTTCAGGGCCGGCA 444
 Db 385 GCCCCGAGCCACCCAGGGTGCATGGGGCTTCGCTCTGGCTTCAGGGCCGGCA 444
 Qy 445 GGAGGGTCCAGTGTGGCTCCATCTGGAGGCTTCCTGGAGGTGTGTAACGGCTCTTA 504
 Db 445 GGAGGGTCCAGTGTGGCTCCATCTGGAGGCTTCCTGGAGGTGTGTAACGGCTCTTA 504
 Qy 505 CGCCACCTGGCCAGCCC 522
 Db 505 CGCCACCTGGCCAGCCC 522

Query Match 93.3%; Score 486.8; DB 1; Length 525;
 Best Local Similarity 98.6%; Pred. No. 2..3e-109;
 Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

25 CTACACAGAGCTCCCTTAAAGCTTAGACAAAGTGGAAAGATCCAGGGATGGC 84
 Db 25 CTGCCAGAGCTCCCTTAAAGCTTAGACAAAGTGGAAAGATCCAGGGATGGC 84
 Qy 145 CTGCTGGGACACTCTGGGATCCCTGGCTGAGGAGCTGCCAGGCC 204
 Db 145 CTGCTGGGACACTCTGGGATCCCTGGCTGAGGAGCTGCCAGGCC 204
 Qy 85 CGAGCGCTCCAGGAGCTGTCAGCTGGCTCCCTGGCTGAGGAGCTGCCAGGCC 204
 Db 85 CGAGCGCTCCAGGAGCTGTCAGCTGGCTCCCTGGCTGAGGAGCTGCCAGGCC 204
 Qy 205 CTGAGCTGGAGGGCTGCTGTGGCAACTCCATAGGGCCCTTTCCTCTAACAGGGCTC 264
 Db 205 CTGAGCTGGAGGGCTGCTGTGGCAACTCCATAGGGCCCTTTCCTCTAACAGGGCTC 264
 Qy 265 CTGAGGCCCTGGAGGGATCTCCCGAGTGTGTCACCTGGACACCTGGAGCTGCCAGGCC 204
 Db 265 CTGAGGCCCTGGAGGGATCTCCCGAGTGTGTCACCTGGACACCTGGAGCTGCCAGGCC 204

SEQUENCE LISTING
-08-783-288-1
Sequence 1, Application US/08783288
Patent No. 5795968
GENERAL INFORMATION:
APPLICANT: KUGA, TETSURO
APPLICANT: MIYAJI, HIROMASA
APPLICANT: SATO, MORIYUKI
APPLICANT: OKABE, MASAMI
APPLICANT: MORIMOTO, MAKOTO
APPLICANT: ITOH, SEIIGA
APPLICANT: YAMASAKI, MOTOZO
APPLICANT: YOKO, YOSHIIHARU
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINOI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,288
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,411
FILING DATE: 03-MAY-1995
APPLICATION NUMBER: JP 306799/86
FILING DATE: 23-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 80088/88
FILING DATE: 31-MAR-1988
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 24-9-73
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
SEQUENCE CHARACTERISTICS:

RESULT 6
US-08-469-318-177
; Sequence 177, Application US/08469318
; Patent No. 602535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariable IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 177:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-469-318-177

RESULT 7
US-08-469-318-178
; Sequence 178, Application US/08469318
; Patent No. 602535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariable IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-469-318-178

Query Match 90.9%; Score 474.6; DB 3; Length 546;
Best Local Similarity 94.4%; Pred. No. 2.1e-16; Mismatches 29; Indels 0; Gaps 0;
Matches 492; Conservative 0; Mismatches 29;

Qy 2 CGCCAAATATCGCCCTCGAGCTCCCTGAGCTCCCTGAGCTTAAAGCTAGACCAAG 61
Db 8 CACCATTAAGCTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAG 67

Qy 62 TGGAGAAGATCCAGGGCAGATGGCGAGCGCAGGATGGCAAGCTGTGCACTAACAGC 121
Db 68 TGGAGAAGATCCAGGGCAGATGGCGAGCGCAGGATGGCAAGCTGTGCACTAACAGC 127

Qy 122 TGTGCCACCCGGAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 181
Db 128 TGTGCCACCCGGAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 187

Qy 182 TGGAGCTGCCAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 181
Db 188 TGGAGCTGCCAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 187

Qy 242 GCCTTTCCTCTACCAAGGGCTCCTACCAAGGGCTCTGGAAAGGGATCTCCCGAGTTGGTC 301
Db 248 GCCTTTCCTCTACCAAGGGCTCTGGAAAGGGATCTCCCGAGTTGGTC 307

Qy 302 CCACCTTGGACACACTGGAGCTGGAGCTGGCCACTTGGCACCACATGGCAGAGA 361
Db 308 CCACCTTGGACACACTGGAGCTGGAGCTGGCCACTTGGCAGAGA 367

Qy 362 TGGAAAGACTGGAAATGGCCTGGCCAGGGCTGGAGCTGGCTGGCTGGCTGG 421
Db 368 TGGAAAGACTGGAAATGGCCTGGCCAGGGCTGGAGCTGGCTGGCTGGCTGG 427

Qy 422 CCTCTGGTTTCAGGCCGGCAAGGGGCTCTAGTTGCCATCTGGCTGGCTGGCTGG 481
Db 428 CCTCTGGTTTCAGGCCGGCAAGGGGCTGGCTGGCTGGCTGGCTGGCTGG 487

Qy 482 TGGAGCTGTTGACCTGGCTACGCCACCTGGCCAGGCC 522
Db 488 TGGAGCTGTTGACCTGGCTACGCCACCTGGCCAGGCC 528

Query Match 90.9%; Score 474.6; DB 3; Length 546;
Best Local Similarity 94.4%; Pred. No. 2.1e-16; Mismatches 29; Indels 0; Gaps 0;
Matches 492; Conservative 0; Mismatches 29;

Qy 2 CGCCAAATATCGCCCTCGAGCTCCCTGAGCTTAAAGCTAGACCAAG 61
Db 8 CACCATTAAGCTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAG 67

Qy 62 TGGAGAAGATCCAGGGCAGATGGCGAGCGCAGGATGGCAAGCTGTGCACTAACAGC 121
Db 68 TGGAGAAGATCCAGGGCAGATGGCGAGCGCAGGATGGCAAGCTGTGCACTAACAGC 127

Qy 122 TGTGCCACCCGGAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 181
Db 128 TGTGCCACCCGGAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 187

Qy 182 TGGAGCTGCCAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 181
Db 188 TGGAGCTGCCAGGAGCTGGCTCTCGGACACTCTCGGACATCCCTGGCTCCC 187

Qy 242 GCCTTTCCTCTACCAAGGGCTCCTACCAAGGGCTCTGGAAAGGGATCTCCCGAGTTGGTC 301
Db 248 GCCTTTCCTCTACCAAGGGCTCTGGAAAGGGATCTCCCGAGTTGGTC 307

Qy 302 CCACCTTGGACACACTGGAGCTGGAGCTGGCCACTTGGCACCACATGGCAGAGA 361
Db 308 CCACCTTGGACACACTGGAGCTGGCCACTTGGCAGAGA 367

Qy 362 TGGAAAGACTGGAAATGGCCTGGCCAGGGCTGGAGCTGGCTGGCTGGCTGG 421
Db 368 TGGAAAGACTGGAAATGGCCTGGCCAGGGCTGGAGCTGGCTGGCTGGCTGG 427

Qy 422 CCTCTGGTTTCAGGCCGGCAAGGGGCTCTAGTTGCCATCTGGCTGGCTGGCTGG 481
Db 428 CCTCTGGTTTCAGGCCGGCAAGGGGCTGGCTGGCTGGCTGGCTGGCTGG 487

Qy 482 TGGAGCTGTTGACCTGGCTACGCCACCTGGCCAGGCC 522
Db 488 TGGAGCTGTTGACCTGGCTACGCCACCTGGCCAGGCC 528

RESULT 8

Sequence 177, Application US/08468609A

Patent No. 6030812

GENERAL INFORMATION:

APPLICANT: Adams, Mark A.

APPLICANT: Bauer, S. C.

APPLICANT: Bradford-Goldberg, Sarah R.

APPLICANT: Caparon, Maire H.

APPLICANT: Easton, Alan M.

APPLICANT: Klein, Barbara K.

APPLICANT: McKearn, John P.

APPLICANT: Olians, Peter O.

APPLICANT: Palk, Kumman

APPLICANT: Thomas, John W.

TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Intelexukin-3 (IL-6)

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,

STREET: P. O. Box 5110

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60680

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,609A

FILING DATE: 06-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314)737-6972

TELEFAX: (314)737-6986

INFORMATION FOR SEQ ID NO: 177:

SEQUENCE CHARACTERISTICS:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLogy: linear

MOLECULE TYPE: DNA (genomic)

US-08-468-609A-177

Query Match 90.9%; Score 474.6%; DB 3; Length 546;

Best Local Similarity 94.4%; Pred. No. 2.1e-10;

Matches 492; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 2 CGGCCACATATGCCGCTCGAGCTTACACAGAGCTTAAANAGCTTAGCAAG 61

Db 8 CACCATTAAGCCCTGGCCAGCTGCTGCCAGAGCTTCTGTCTAGCAG 67

Qy 62 TGAGGAAGTCAGGGATGGGGTCAAGGAAGCTGTGCACTTAGAGC 121

Db 68 TGAGGAAGTCAGGGATGGGGTCAAGGAAGCTGTGCACTTAGAGC 127

Qy 122 TGTGCAACCCGAGGAGCTGCTGCTGGCAACTCTGGCAGTGGCC 181

Db 128 TGTGCAACCCGAGGAGCTGCTGCTGGCAACTCTGGCAGTGGCC 187

Qy 182 TGAGCAGTCAGGCCAGCCAGGCCCTGCAAGCTGCTGTGAGCCAACTCCATAGCG 241

RESULT 9

US-08-468-609A-178

Sequence 178, Application US/08468609A

Patent No. 6030812

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

APPLICANT: Bauer, S. C.

APPLICANT: Bradford-Goldberg, Sarah R.

APPLICANT: Caparon, Maire H.

APPLICANT: Easton, Alan M.

APPLICANT: Klein, Barbara K.

APPLICANT: McKearn, John P.

APPLICANT: Olians, Peter O.

APPLICANT: Paik, Kumanan

APPLICANT: Thomas, John W.

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,

STREET: P. O. Box 5110

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60680

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,609A

FILING DATE: 06-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314)737-6972

TELEFAX: (314)737-6986

INFORMATION FOR SEQ ID NO: 177:

SEQUENCE CHARACTERISTICS:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLogy: linear

MOLECULE TYPE: DNA (genomic)

US-08-468-609A-177

Query Match 90.9%; Score 474.6%; DB 3; Length 546;

Best Local Similarity 94.4%; Pred. No. 2.1e-10;

Matches 492; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 2 CGGCCACATATGCCGCTCGAGCTTACACAGAGCTTAAANAGCTTAGCAAG 61

Db 8 CACCATTAAGCCCTGGCCAGCTGCTGCCAGAGCTTCTGTCTAGCAG 67

Qy 62 TGAGGAAGTCAGGGATGGGGTCAAGGAAGCTGTGCACTTAGAGC 121

Db 68 TGAGGAAGTCAGGGATGGGGTCAAGGAAGCTGTGCACTTAGAGC 127

Qy 122 TGTGCAACCCGAGGAGCTGCTGCTGGCAACTCTGGCAGTGGCC 181

Db 128 TGTGCAACCCGAGGAGCTGCTGCTGGCAACTCTGGCAGTGGCC 187

Qy 182 TGAGCAGTCAGGCCAGCCAGGCCCTGCAAGCTGCTGTGAGCCAACTCCATAGCG 241

CLASSIFICATION:

PATENT APPLICATION DATA:

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314)737-6986

TELEFAX: (314)737-6972

INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-468-509A-178

Query Match 90.9%; Score 474.6; DB 3; Length 546;
 Best Local Similarity 94.4%; Pred. No. 2.1e-106;
 Matches 492; Conservative 0; Mismatches 29; Indels 0; Caps 0;

Qy 2 CGCCAAACATATCGCSCCTCGAGTCGAGCTTACACAGAGCTCCCTTTAAAGGTTAGCAAG 61
 Db 8 CACCATTAAGACCTTCGACGCCCTCCAGAGCTTCGGCTCAAGTGGTTAGCAAG 67
 Qy 62 TGGAGGAGATTCAGGGAGATTCAGGGCAGTGGCAGGGCTCAGAGAAGCTGTGCACTCAAGC 121
 Db 68 TGGAGGAGATTCAGGGCAGATGGCAGGGCTCAGAGAAGCTGTGCACTCAAGC 127
 Qy 122 TGTGCCACCCGGAGGAGCTGGCTCGAGACACTCTCTGGCATCCCTGGCTCCCC 181
 Db 128 TGTGCCACCCGGAGGAGCTGGCTCGAGACACTCTCTGGCATCCCTGGCTCCCC 187
 Qy 182 TGGAGGAGATTCAGGGAGATTCAGGGCAGTGGCAGGGCTCAGAGAAGCTGTGCACTCAAGC 241
 Db 188 TGGAGGAGATTCAGGGAGCTGGCTCGAGACACTCTCTGGCATCCCTGGCTCCCC 247
 Qy 242 GCCTTTTCCCTACAGGGGCTCCAGGGGAGATTCAGGGCAGTGGGTC 301
 Db 248 GCCTTTTCCCTACAGGGGCTCCAGGGGAGATTCAGGGCAGTGGGTC 307
 Qy 302 CACACCTGGACACACTGGAGCTGGGAGCTGGCACCATCTGGCAGA 361
 Db 308 CCACCTTGGAACACTGGAGCTGGGAGCTGGCACCATCTGGCAGA 367
 Qy 362 TGGAAAGAACTGGGAAATGGCCCTGCGCCCTGCGCCCTGGCAGA 421
 Db 368 TGGAAAGAACTGGGAAATGGCCCTGCGCCCTGGCAGA 427
 Qy 422 CCTCGTGCTTCAGGGGAGATGGGCTCCATGGGAGCTGGCAGTGGCAGACTTC 481
 Db 428 CCTCGTGCTTCAGGGGAGATGGGCTCCATGGGAGCTGGCAGACTTC 487
 Qy 482 TGGAGGTGTGTACCCGGCTACGCCACCTTGCCAGGCC 522
 Db 488 TGGAGGTGTGTACCCGGCTACGCCACCTTGCCAGGCC 528

RESULT 10 PCT-US95-01185-178

Sequence 177, Application PC/TUS9501185

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Multivariable IL-3 Hematopoiesis Fusion

NUMBER OF SEQUENCES: 196

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01185

FILING DATE: 02-FEB-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192325

INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-01185-177

Query Match 90.9%; Score 474.6; DB 5; Length 546;
 Best Local Similarity 94.4%; Pred. No. 2.1e-106;
 Matches 492; Conservative 29; Mismatches 0; Indels 0; Caps 0;

Qy 2 CGCCACATATCGCSCCTCGAGTCGAGCTTACACAGAGCTCCCTTTAAAGGCTTAGCAAG 61
 Db 8 CACCATTAAGACCTTCGACGCCCTCCAGAGCTTCGGCTCAAGTGGCTTAGCAAG 67
 Qy 62 TGGAGGAGATTCAGGGGAGATGGCAGGGCTCAGAGAAGCTGTGCACTCAAGC 121
 Db 68 TGGAGGAGATTCAGGGCAGATGGCAGGGCTCAGAGAAGCTGTGCACTCAAGC 127
 Qy 122 TGTGCCACCCGGAGGAGCTGGCTCGAGACACTCTCTGGCATCCCTGGCTCCCC 181
 Db 128 TGTGCCACCCGGAGGAGCTGGCTCGAGACACTCTCTGGCATCCCTGGCTCCCC 187
 Qy 182 TGGAGGAGATTCAGGGGAGATTCAGGGCAGTGGCAGGGCTCAGAGGCTGTGCACTCAAGC 241
 Db 188 TGGAGGAGATTCAGGGGAGCTGGCTCGAGACACTCTCTGGCATCCCTGGCTCCCC 247
 Qy 242 GCCTTTTCCCTACAGGGGCTCCAGGGGAGATTCAGGGCAGTGGGTC 301
 Db 248 GCCTTTTCCCTACAGGGGCTCCAGGGGAGATTCAGGGCAGTGGGTC 307
 Qy 302 CACACCTGGACACACTGGAGCTGGGAGCTGGCACCATCTGGCAGA 361
 Db 308 CCACCTTGGAACACTGGAGCTGGGAGCTGGCACCATCTGGCAGA 367
 Qy 362 TGGAAAGAACTGGGAAATGGCCCTGCGCCCTGCGCCCTGGCAGA 421
 Db 368 TGGAAAGAACTGGGAAATGGCCCTGCGCCCTGGCAGA 427
 Qy 422 CCTCGTGCTTCAGGGGAGATGGGCTCCATGGGAGCTGGCAGACTTC 481
 Db 428 CCTCGTGCTTCAGGGGAGATGGGCTCCATGGGAGCTGGCAGACTTC 487
 Qy 482 TGGAGGTGTGTACCCGGCTACGCCACCTTGCCAGGCC 522
 Db 488 TGGAGGTGTGTACCCGGCTACGCCACCTTGCCAGGCC 528

RESULT 11 PCT-US95-01185-178

Sequence 178, Application PC/TUS9501185

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Multivariable IL-3 Hematopoiesis Fusion

NUMBER OF SEQUENCES: 196

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01185

FILING DATE: 02-FEB-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192325

INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

Query Match 90.9%; Score 474.6; DB 5; Length 546;
 Best Local Similarity 94.4%; Pred. No. 2.1e-106; Indels 0; Gaps 0;
 Matches 492; Conservative 0; Mismatches 29; Gaps 0;

Query Match 90.9%; Score 474.6; DB 3; Length 921;
 Best Local Similarity 94.4%; Pred. No. 2.1e-106; Indels 0; Gaps 0;
 Matches 492; Conservative 0; Mismatches 29; Gaps 0;

Qy 2 CGCCAAACATATGCCCTCGAAGCTCCTTAAAGCTTAGAGCAAG 61
 Db 8 CACCATAGAACCTGCCAGCTGCCAGAGCTCTGCAGTCAGCAAG 67

Qy 62 TGAGAAAGATCAGGGATGGGGCAGGGCTCAGGAAGGGTGTGCAACCTAACAGC 121
 Db 68 TGAGAAAGATCAGGGATGGGGCAGGGCTCAGGAAGGGTGTGCAACCTAACAGC 127

Qy 122 TGTGCCACCCGAGGCTGTCGTGGACACTCTGGCATCCPGGTCCCC 181
 Db 128 TGTGCCACCCGAGGCTGTCGTGGACACTCTGGCATCCPGGTCCCC 187

Qy 182 TGAAGAGCTGCCAGGGCTGGAGCTGGCTGAGGCAACTCCATAGCG 241
 Db 188 TGAAGTCTGCCAGGGCTGGAGCTGGCTGAGGCAACTCCATAGCG 247

Qy 242 GCCATTTCCTCTACCGGGCTCTGGAGGGTGTCTGGGACTCTCTGGCATCCGGTCCCC 301
 Db 248 GCCATTTCCTCTACCGGGCTCTGGAGGGTGTCTGGGACTCTCTGGCATCCGGTCCCC 307

Qy 302 CACACTGGACACACTGGAGCTGGACCTGGCCGACTCTGGCAGCAGA 361
 Db 308 CACACTGGACACACTGGAGCTGGACCTGGCCGACTCTGGCAGCAGA 367

Qy 362 TGAAGAACTGGGATGCCCTGGCCCTGGAGCCACGGGTGCCATGGGGCTTCG 421
 Db 368 TGAAGAACTGGGATGCCCTGGCCCTGGAGGGTATGCCGGCTTCG 427

Qy 422 CCTCTGGTTTCAAGCGGGGGAGGGGGCTCTAGTGGCTCCATGGAGGCTTC 481
 Db 428 CCTCTGGTTTCAAGCGGGGGAGGGGGCTCTAGTGGCTCCATGGAGGCTTC 487

Qy 482 TGGAGGTGTGTGTACTGGCCTTCAAGCCACCTTGCCCAAGCCC 522
 Db 488 TGGAGGTGTGTACTGGCCTTCAAGCCACCTTGCCCAAGCCC 528

RESULT 12
 US-08-469-318-72
 Sequence 72, Application US/08469318
 ; Patent No. 6022535

GENERAL INFORMATION:

APPLICANT: ; TITLE OF INVENTION: Multivarient IL-3 Hematopoiesis Fusion
 ; TITLE OF INVENTION: Protein
 ; NUMBER OF SEQUENCES: 196

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/469,318
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/446,872
 ; FILING DATE:
 ; INFORMATION FOR SEQ ID NO: 72:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 921 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)

US-08-469-318-75

Query Match 90.9%; Score 474.6; DB 3; Length 921;

Oy	2	GCCAAACATATCGCCCTCGAGTCACCAAGAGCTTAAAGCTAGAGAAG	61
Db	401	ACCAATTAGCCCTGCCAGCTCCCTGCCAGAGCTCTGCTCAATGCTAGAGC	460
Oy	62	TGAGGAAGATCAGGGATGCGCTGGCGAGCTGGAGAAAGCTGTGCCACCTACAAGC	121
Db	461	TGAGGAAGATCAGGGATGCGCTGGAGCTGGCGAGCTGGAGAAAGCTGTGCCACCTACAAGC	520
Oy	122	TGTGCACCCGAGGAGCTGCTGCGAGGACACTCTGGCATCCCTGGCCTCCC	181
Db	521	TGTGCCACCCGAGGAGCTGGCTGCGAGGACACTCTGGCATCCCTGGCCTCCC	580
Oy	182	TGAGAGCTGCCAGCCAGCCATGCGAGCTGCAAGCTTGAGCCAACCTCATAGG	241
Db	581	TGAGETCCGCCAGCCAGGCCCTGCAAGCTGGCTGAGCTGGCAGGCTGAGCCAACTCCATAGG	640
Oy	242	GCCTTTCTCTTACAGGGCTCTGCAAGCCCTGGAGGGATCTCCCGAGTTGGTC	301
Db	641	GCCTTTCTCTTACAGGGCTCTGCAAGCCCTGGAGGGATCTCCCGAGTTGGTC	700
Oy	302	CAACCTTGGACACACTGCAAGCTGCGCAACTTGTGCCACCACTTGCGAGAGA	361
Db	701	CAACCTTGGACACACTGCAAGCTGCGCAACTTGTGCCACCACTTGCGAGAGA	760
Oy	362	TGGAGAACTGGAAATGGCACTGGCCCTGCCCTGGAGCCACCCAGGGCCATGGCCCTTCG	421
Db	761	TGGAGAACTGGAAATGGCCCTGCCCTGGAGCCACCCAGGGCTGCCATGGCCCTTCG	820
Oy	422	CCTCGCTTTCAGGGGGAGGGGGCTAGTGGCCACACTGAGAGCTTCC	481
Db	821	CCTCGCTTTCAGGGGGAGGGTCTGGTGGCTAGCCACATCTGGAGCTTCC	880
Oy	482	TGGAGGTGCTGTAAGCGGTTAGCCACCTTGCCACCC	522
Db	881	TGGAGGTGCTGTAAGCGGTTAGCCACCTTGCCACCC	921

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2002, 08:59:09 ; search time 262.13 Seconds
(without alignments)
3419.026 Million cell updates/sec

Title: US-09-680-514-4_COPY_526_1047

Perfect score: 522

Sequence: 1 GGGCAAACATATCGGCCTC.....TACGCCACCTTGCCCAAGCCC 522

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters : 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Genesed_033802:*

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2: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA1981 DAT:*

3: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA1982 DAT:*

4: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA1983 DAT:*

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22: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2001A DAT:*

23: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2001B DAT:*

24: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2002 DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match	Length	DB ID	Description
1	522	100 0	1047	17	AAT41786		Fusion peptide #1
2	522	100 0	1095	17	AAT41788		Fusion peptide #3
3	520.4	99 7	1083	17	AAT41787		Fusion peptide #2
4	514	98 5	525	11	AAQ04482		Plasmid pASN6 enco
5	510.8	97.9	525	11	AAQ04484		Plasmid pASN145 en
6	506	96.9	525	11	AAQ04481		Plasmid pAS28 enco
7	486.8	93.3	525	9	AAQ04487		hG-CSF gene isolate
8	486.8	93.3	531	22	AAD1972		Human hG-CSF gene
9	486.8	93.3	615	22	AAD1971		Human hG-CSF gene

10	486.8	93.3	1520	8	AAN70223	Plasmid pBRY2 ins
11	486.8	93.3	1520	8	AAN71320	Sequence encoding
12	486.8	93.3	1521	7	AAN60937	Plasmid pBRY2 ins
13	486.8	93.3	1525	9	AAN81478	Sequence encoding
14	486.8	93.3	1525	10	AAN91086	Plasmid pP12 contg
15	485.2	93.0	1415	8	AAN91089	Sequence of human
16	484.2	92.8	644	22	API71848	Recombinant human
17	474.6	90.9	546	16	APQ97205	PMON13499 DNA sequ
18	474.6	90.9	546	16	APQ97205	PMON13010 DNA sequ
19	474.6	90.9	546	21	AAQ03772	Human G-CSF mutant
20	474.6	90.9	546	21	AAQ03773	Human G-CSF mutant
21	474.6	90.9	921	21	AAQ97186	PMON13026 DNA enco
22	474.6	90.9	921	16	AAQ97189	PMON13043 DNA enco
23	474.6	90.9	923	20	AAQ97190	PMON13066 DNA enco
24	474.6	90.9	921	16	AAQ97192	PMON13058 DNA enco
25	474.6	90.9	921	21	AAQ97194	Human interleukin-
26	474.6	90.9	921	21	AAQ97195	Human interleukin-
27	474.6	90.9	921	21	AAQ97196	Human interleukin-
28	474.6	90.9	921	21	AAQ97197	Human interleukin-
29	474.6	90.9	921	20	AAQ97198	Human granulocytic
30	474.6	90.9	966	16	AAQ97198	PMON13060 DNA enco
31	474.6	90.9	966	16	AAQ97198	PMON13063 DNA enco
32	474.6	90.9	966	16	AAQ97198	PMON13045 DNA enco
33	474.6	90.9	966	16	AAQ97191	PMON13152 DNA enco
34	474.6	90.9	966	16	AAQ97193	PMON13152 DNA enco
35	474.6	90.9	966	16	AAQ97194	Human interleukin-
36	474.6	90.9	966	21	AAQ03736	Human interleukin-
37	474.6	90.9	966	21	AAQ03738	Human interleukin-
38	474.6	90.9	966	21	AAQ03739	Human interleukin-
39	474.6	90.9	966	21	AAQ03741	Human interleukin-
40	474.6	90.9	966	21	AAQ03745	Human interleukin-
41	474.6	90.9	966	21	AAQ03747	Human interleukin-
42	474.6	90.9	1017	16	AAQ97181	PMON15937 DNA enco
43	474.6	90.9	1017	21	AAQ03735	Human granulocytic
44	474.6	90.9	1047	16	AAQ97188	PMON13064 DNA enco
45	474.6	90.9	1047	16	AAQ97190	PMON13044 DNA enco

ALIGNMENTS

RESULT 1
AAT41786 standard; DNA; 1047 BP.
XX
ID AAT41786
XX
AC
DT 01-JUL-1997 (first entry)
XX
DE Fusion peptide #1 having G-CSF and TPO activity.
XX
KW Fusion protein; human granulocyte colony stimulating factor; hG-CSF;
KW thrombopoietin; TPO; spacer peptide; blood platelet production;
KW leukocyte production; anaemia; ds.
XX
OS Homo sapiens.
XX
KW
XX
Key
FT sig_peptide
FT mat_peptide
FT /*tag= a
FT /*tag= b
XX
PN W09634016-A1.

RESULT	9
AADD19771	
ID	AADD19771 standard; DNA; 615 BP.
XX	
AC	AADD19771;
AC	
XX	18-DEC-2001 (first entry)
DT	DT
XX	Human hg-CSF gene inserted into plasmid p19GCSFm.
DE	
XX	
KW	Human; granulocyte colony stimulating factor; hg-CSF; protease
KW	Factor Xa; kanamycin resistance; endoxylanase signal peptide; c
XX	
XX	Homo sapiens.
OS	
OS	
XX	Key
FH	Location/Qualifiers
FT	88..612
FT	/tag= a
FT	/product= "Human hg-CSF protein"
FT	/note= "CDS does not include start codon"
FT	/partial

PN	WO200173081-A1.
XX	
PD	04-OCT-2001.
XX	
PF	31-MAR-2001; 2001WO-KR000549.
XX	
PR	31-MAR-2000; 2000KR-0017052.
XX	
PA	(KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX	
PI	Lee S, Jeong K;
XX	
DR	WPI; 2001-616523/71.
XX	
DR	P-PSDB; AAE12153/71.
XX	
PT	Recombinant plasmid vector comprising an endoxylanase signal
PT	human granulocyte colony stimulating factor gene and other comp-
PT	when transformed into microorganism useful for preparing the co-
PT	stimulating factor -
PT	
XX	
PS	Example 1; Fig 3; 50pp; English.
XX	
CC	The invention relates to an <i>Escherichia coli</i> producing and sec-

human granulocyte colony stimulating factor (hG-CSF), more specifically, to a recombinant plasmid constructed to express secretory hG-CSF in *E. coli*, an *E. coli* transformed with that plasmid to secrete hG-CSF, and a process for preparing hG-CSF using the transformed hG-CSF. The recombinant plasmid vector comprises of a kanamycin resistance gene, a promoter, an endoxylanase signal sequence, a nucleotide sequence coding for an oligopeptide consisting of 13 amino acids including 6 consecutive histidine residues and a hG-CSF. *E. coli* transformed with recombinant plasmid vector is useful for preparing hG-CSF. The method comprises culturing the microorganism to obtain a hG-CSF fusion protein and treating the fusion protein with a protease preferably Factor Xa, to obtain a hG-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is human hG-CSF gene inserted into plasmid p19CSM.

XX WPI, 1987-064855/09.
XX p-PSDB; AAP7030.

XX Poly: peptide with granulocyte colony stimulating factor activity
- obt. by recombinant DNA procedures for treating haemopoietic
- a.

xx Disclosure; Page 22-24; 79pp; English.
xx The examples describe procedures for the designing of probes for
xx hpg-CSF cDNA and genomic clones, both of which are claimed.

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		BB598945		P11_84_E1	
c	18	43.2	8.3	461	10
c	19	43.2	8.3	559	10
c	20	42.6	8.2	552	9
c	21	42.6	8.2	899	12
c	22	42.4	8.1	1203	12
c	23	42.2	8.1	1205	12
c	24	41.4	7.9	598	9
c	25	41.4	7.9	421	9
c	26	41.2	7.9	478	10
c	27	40.8	7.8	676	9
c	28	40.8	7.8	545	10
c	29	40.8	7.8	893	10
c	30	40.6	7.8	1011	10
c	31	40.6	7.8	447	10
c	32	40.6	7.8	845	9
c	33	40.6	7.8	12	CNS072Q
c	34	40.4	7.7	1003	10
c	35	40.4	7.7	10	B14.10408
c	36	40.4	7.7	458	9
c	37	40	7.7	9	AW273202
c	38	40	7.7	485	10
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c	40	39.8	7.6	485	10
c	41	39.8	7.6	485	10
c	42	39.8	7.6	864	12
c	43	39.8	7.6	368	10
c	44	39.8	7.6	548	10
c	45	39.8	7.6	507	10
c	46	39.8	7.6	387	9
c	47	39.8	7.6	427	9
c	48	39.8	7.6	404	8
c	49	39.8	7.6	432	9
c	50	39.8	7.6	441	9
c	51	39.8	7.6	441	9
c	52	39.8	7.6	450	9

ALIGNMENTS

RESULT	1	ORGANISM	<i>Homo sapiens</i>
BM423896	BM423896	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
LOCUS	AGENCOURT_6399123	990 bp	
DEFINITION	5' mRNA sequence.	mRNA	
ACCESSION	BM423896	NIH_MGC_41	
VERSION	BM423896.1	<i>Homo sapiens</i> cDNA clone IMAGE:5517129	
KEYWORDS	EST.		
SOURCE	human.		
REFERENCE	1 (bases 1 to 990)		
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		

Tissue Procurement: DCID/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLMCM2018 row: n column: 10
 High quality sequence stop: 542.
 Location/Qualifiers
 1. 990
 source
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 /db_xref="taxon:9606"
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 /clone_lib="NH_MGC_41"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pGEM7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California

Description	BM433896 AGENCEOURT
	BM009358 603629823
	BI9608124 MONOI_7_G
	BI9608124 MONOI_1_B
	BI411.28 60296472
	BG58320 602575289
	BE45194 171120_BA
	BM009124 603629863
	BI822673 603036006
	BI961002 MONOI_3_H
	BM252621 518592_MA
	BF848766 QVO-#NO10
	BI961982 MONOI_7_G
	AL053013 drosophil
	BE480590 165716_BA
	AL053013 drosophil
	AI985598 rat_pk006

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

result		Query	Score	Match	Length	DB	ID
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	2	387..8	74.3	817	10	BM009358	
	3	343..6	65.8	570	10	B1961242	
	4	323..6	62.0	548	10	B1960812	
	5	320..4	61.4	973	10	B1411128	
	6	312..8	59.9	598	10	BG548320	
	7	300..6	57.6	507	10	BE485194	
	8	281..2	53.9	829	10	BM000247	
	9	210..6	40.3	948	10	B1822673	
	10	181..	34.7	368	10	B1961002	
	11	150..	28.7	509	10	BM25261	
	12	135..8	26.0	327	10	BF84866	
	13	67.8	13.0	673	10	B1961882	
	14	54.8	10.5	925	12	CNS0091P	
	15	50..2	9.6	513	10	BE480590	
	16	44..9	9.4	925	12	CNS0091P	
c	17	48..8	9.3	617	9	A198158	

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295	CTGCCAGAGCTTCCTGCTCAAGTCCTTGTAGCAAGTGGAGAATCCAGGGCGATGGC	354				
85	GCAGGCTTCAGAGAAGCTGTGACCTACAGTGTGCCAACCTACAGTGTGCCAACCTACAGTGTGCCAACCCAGGAGCTGGTGT	144				
355	GCAGGCTTCAGAGAAGCTGTGACCTACAGTGTGCCAACCCAGGAGCTGGTGT	414				
145	CTGTCGGACACTCTCTGGCATCCCTGGCTCCCTGGCTCCAGCAGTGCCTGCCAGGCC	204				
415	CTGTCGGACACTCTCTGGCATCCCTGGCTCCCTGTGACCTGTGCCAGGCC	474				
205	CTGCAAGTGGCAGGCTCTGGCATCCACTCCATAGGGCTTTCCTACCAAGGGCTC	264				
475	CTGCAAGTGGCAGGCTCTGGCATCCACTCCATAGGGCTTTCCTACCAAGGGCTC	534				
265	CTTGAGGGCCTGAAAGGATCTCCCGAAGTGGTGTCCACCTTGACACTGAGCTG	324				
535	CTTGAGGGCCTGAAAGGATCTCCCGAAGTGGTGTCCACCTTGACACTGAGCTG	594				
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595	GAGTCGGCAGACTTGGCACCACCTGTCAGGAGACTGGAAATGGCCCT	654				
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655	GCGCTGAGGCCACCCAGGGGCGCATGGCCATGGCCGGCCTTGCGCTCTGCTTCCAGGCCGGC	714				
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715	AGGGGGCTCTGGTGTCTGGAGGTCTACCGGTCTGGAGGTCTACCGGTCT	774				
504	ACGCCACCTTGCCCAAGC 521					
775	ACGCCACCTTGCCCAAGC 792					
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ACCESSION	BM009358					
VERSION	BM009358.1					
KEYWORDS	EST.					
SOURCE	human					
ORGANISM	Human					
Eukaryota	Metazoa	Chordata	Caniata	Vertebrata	Euteleostomi	
Mammalia	Buterilia	Primates	Catarrhini	Hominidae	Homo.	
REFERENCE	1 (bases 1 to 817)					
AUTHORS	NIH_MGC	http://mgc.ncbi.nih.gov/				
TITLE	National Institutes of Health	Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D.					
	Email: cgsbsr@mail.nih.gov					
	Tissue Procurement: DCND/DRP					
	CDNA Library Preparation: Ling Hong/Rubin Laboratory					
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:					
	http://image.llnl.gov					

REFERENCE	FEATURES	source
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
1 (bases 1 to 570)		
Vandenplas, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E.,		
Gingle, A.R., Pratt, L.H. and Moore, J.N.		
An EST database from equine (<i>Equus caballus</i>) monocytes		
Unpublished (2001)		
Contact: Cordonnier-Pratt MM		
Department of Botany		
The University of Georgia		
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA		
TeI: 706 542 1860		
Fax: 706 542 1805		
Email: mprratt@uga.edu		
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyTM or T7 sequencing primer, are presented as the reverse complement.		
Seq. primer: JEN REV		
High quality sequence stop: 541		
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	/db_xref="Taxon:9796"	
	/clone_lib="Monocytes (MONOL)"	
	/cell_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"	
	/note="Vector: pBluescript SK(-) from Lambda ZAPII;	
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100 a	100 c	167 g 101 t
BASE COUNT		
OPTICN		

/note="Organ: skin; Vector: pOTB7; Site_1: XbaI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACTGG (G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supercript II RT (Life Technologies). Note: this is a NIH_MCG Library."
131 a 297 c 248 g 153 t

Query	Match	53.9%	Score 281.2;	DB 10;	Length 829;
Best Local	Similarity	82.5%	Pred. No.	1-2e-53;	
Matches	421;	Conservative	0;	Mismatches	73;
				Indels	16;
				Gaps	8;
Qy	25	CTTACCACTAGAGCTTCCTT-	-TTTAAAAGCTTAGAGCAAGT	GAGAAATCCAGGGC	GATG 82
Db	300	CTTCCCTCCAGAGCTTCCTG	CCAAATGCTTAGAGCAAGT	GAGAAATCCAGGGC	GATG 359
Qy	83	GCCAGGCCTCAGGAACTGTG	CACCTAACCTAACGGCTG	GCCACCCGGAGGAGCT	G 142
Db	360	GCCAGGCCTCAGGAACTGTG	CTGCAAGTTACAGCTG	GGACCTCCAGGAGCTG	36 419
Qy	143	TGTCTGCGGACACTT-	-CTGGGCACTTCCTGGCTC	CTGAGCTTCCAGG	CTCCAGCCA 200
Db	420	TGTCTGCGGACACTTCTG	GGCTCCTTGGGACTCTT	AGCTTCCAGGCT	CTCCAGCCA 479

Qy	201	GGCCCTGAGCTGG - - CAGGTGTTGTAGGCCAACTCATAGGCCCTTTCCTCTACCA	257
Db	480	GGCCCTGAGCTGGCAGGGTGGCTGTGTTGAGCCAACTCATAGGCCCTTTCCTCTACCA	539
Qy	258	GGGGCTCTGAGGCTGGAGGATCTCCCCGAGTGGTCCCACCTGGACACACT	317
Db	540	GGGGCTCTGAGGCTGGAGGATCTCCCCGAGTGGTCCCACCTGGACACACT	599
Qy	318	GCAGCTGAGCTGCC - - ACTTGGCACACCATCTGGAGCAGATGGAACTGGAA	376
Db	600	GCAGCTGAGCTGCCACTTGGCACACCATCTGGAGCAGATGGAACTGGCC	659
Qy	377	TGCCCCCTGCTCTGAGCCACCCAGGGTGCATCGCCGCTTCGCCTC - TGCCTTTCGAG	435
Db	650	ATGGCCCTGCTCTGCA - - CCCACCTGGCTGCATCGCCGCTTCGCCTTCGAG	716
Qy	436	CGGC - - CGGGCAGGAGGGCTCTAGTGGAGCTCCACCTGGAGGT - GTC	491
Db	717	CGCCCGCCACACCGGGCTGCCATCTGAGAGCTTCTGGAGGT - GTC	776
Qy	492	GTACCCGGCTTCTAGGCCACCTGGCCAGCC	521
Db	777	GTACCCGGCTTCTAGGCCACCTGGCCAGCC	806

RESULT 9 BI22673 LOCUS BI22673 LINEAR EST 04-OCT-2001

ACCESSION	B1822673		
VERSION	B1822673.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
COMMENT	mRNA sequence.		
REFERENCE	1. (bases 1 to 948)		
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	unpublished (1999)		
CONTACT	Contact: Robert Strausberg, Ph.D.		
EMAIL	caapbs-r@mail.nih.gov		
TISSUE	Procurement: Life Technologies, Inc.		
CDNA LIBRARY PREPARATION	Life Technologies, Inc.		

FEATURES	source
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov
Plate:	LLM1441 row: k column: 02
High quality sequence stop:	845.
Location/Qualifiers	
1.	948 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE_5177209" /clone_llib="NIH_MGC_1115" /lab_host="DH10B" /note="Organ: pooled brain, lung, testis; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); source anonymous pool of 6 male brains, age range 23-27 male lung, age 27; and 1 male testis, age 6. Library oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb insert size range 1-3 Kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
181 a	301 c 259 g 167 t
BASE COUNT	
ORIGIN	

DEFINITION	Q00-EN0102-081100-45B-906 EN0102 Homo sapiens cDNA, mRNA sequence.	VERSION	BI961882.1	GI	16320085
VERSION	BF848766	EST.			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	<i>Homo sapiens</i>				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nogueira,A., da Silva,W., Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	AUTHORS	Vanderplas,M.L., Cordonnier-Pratt,M.-M., Sudman,M.L., Wentzel,V.E., Gingle,A.R., Pratt,L.H. and Moore,J.M.	REFERENCE	1 (bases 1 to 673)
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	JOURNAL				
2020/663	COMMENT				
Sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Laboratory of Cancer Genetics	Contact: Simpson A.J.G.				
Ludwig Institute for Cancer Research					
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil					
tel: +55-11-2704922					
Fax: +55-11-2707001					
Email: asimpson@ludwig.org.br					
This sequence was derived from the FAPESP/LIGR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QY0-EN0102-081100-45B-906&t=2000-11-08&t4=1)					
seq primer: puc 18 forward					
High quality sequence stop: 327.					
Location/Qualifiers					
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organism="Homo sapiens"					
/db_xref="taxon:606"					
/dev_stage="Adult"					
/clone_lib="EN0102"					
/note="Organ: lung_normal; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
source					
1.					
organism="Homo sapiens"					
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/note="Organ: lung_normal; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
BASE COUNT	61 a 187 c 103 g 76 t	ORIGIN			
Query Match	26.0%	Score	135.8;	DB	10;
Best Local Similarity	89.6%	Pred. No.	7e-21;		
Matches	146;	Conservative	0;	Mismatches	17;
				Indels	0;
				Gaps	0;
201	GGCCCTGAGCTGGAGCTGGCTTCTCTTACAGGG	260	RESULT	14	CNS0091P
Db	139 GGCCCATACAGGCCGGCTGTTGAGCACTCATGGCCTTCTCTTACAGGG	198	LOCUS		CNS0091P
Qy	261 GCTCCCTGAGCCGGCCGAGGATCTCCGGAGTGGTCCACCTGGACACACTGCA	320	DEFINITION		Drosophila melanogaster genome survey sequence TER3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
Db	199 GCTCCCTGAGCCGGCCGAGGATCTCCGGAGTGGTCCACCTGGACACACTGCA	258	ACCESSION	AL053013	AL053013.1
Qy	321 GCTGAGCTGGCCGACTTGGCACCATCTGGAGAGTG	363	VERSION		GI:4934461
Db	259 GCTGAGCTGGCCGACTTGGCACCATCTGGAGAGTG	301	KEYWORDS		GSS.
RESULT	13	ORGANISM			Drosophila melanogaster
BI961882		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.	REFERENCE		Genosope.
LOCUS	BI961882	673 bp	TITLE		Direct Submission
DEFINITION	MONO1_7_G12_91_A005	mRNA	JOURNAL		Submitted (02-JUN-1999) Genoscope - Centre National de Sequencing et de Genotyperie (E-mail : seqref@genoscope.cnrs.fr)
ACCESSION	BI961882	linear	EST	22-OCT-2001	BP 191 91006 ERY cedex

COMMENT	FEATURES	source	BASE COUNT	ORIGIN
<p>- Web : www.genoscope.cns.fr/</p> <p>Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Maimanov in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2, cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.</p>	<p>Location/Qualifiers</p> <p>1 . 925</p> <p>/organism="Drosophila melanogaster" /db_xref="Taxon:7227" /clone_id="RPCI-98" /clone="BACR19D16" /note="end : TE13"</p>	<p>120 a 61 c 61 9 172 t 511 others</p>		

Query Match	Score	DB	Length
Best Local Similarity	10.5%	DB 12;	925;
Matches	15.5%;	Pred. No. 0.019;	
Matches	66;	Conservative	174;
Qy	30	ACAGACCTCTTTAAAAGCTTAGCAGTGTAGGAAAGATCCAGGGATGGCCAGC	89
Db	492	ANANNNTTTATTANNN	551
Qy	90	GCTCCAGGAGAGCTGTGCAACCTACAAGTGTGCCACCCAGGAGCTGTGTGTCT	149
Db	552	TTTSSSGYKGKSSSSGBSCCCSSCCSSCCSSCCSSCCSSCCSSCCSSSSKCS	611
Qy	150	CGGACACTCTGGCATCCCTGGCTCCCTGAGAGCTGCCACCCAGGGCCCTCA	209
Db	612	STSBSSCCCSSKSVGTCSSSSSSSSSSTSSTSSTSSTSSTSSTSSTS	671
Qy	210	GCTGGCAGGCGTGTAGCAACTCTAGCGCCCTTCTACAGGGGGTCTCGCA	269
Db	672	SKSTSASGSWSAGGGSGSTSSSSSSSTSSTSSTSSTSSTSSTSSTS	731
Qy	270	GGCCCTGGAAAGGGATCTCCCCGAGTGGTCCACCTTGGCACACTGCA	326
Db	732	SSSSSTSBBCTSTSSTSSTSSTSSTSSTSSTSSTSSTSSTSSTS	791
Qy	327	CGTCGCGGACATTGGACCAACCACTTGGACAGATGGAAAGACTGGGATGGCC	386

Db	792	YGTSSSSDSTTCCS3CCCYMCTCCS3TYBMCY7TSTS3CGGSSSSSGKAGT7TKCCGGC3SS	851
Qy	387	CTGCAAGCCACCCAGGTGCAATGGGCTTCGCTCTGCTTTCAGCGGGCAGG	446
Db	852	STNGMEGTSAGSSSSSSSSVSSSSKSSSSVSSSGGVS3SSASKSSSSS	911

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Bovinae; Bos.
Bovidae: Bovinae; Bos.
1 (bases 1 to 513)
Sonstegard, T.S., Capuco, A.V., van Tassell, C.P., Ashwell, M.S. and
Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000).
Contact: Sonstegard, TS
USDA, ARS, Beltsville Agricultural Research Center
Bd19, 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadsbpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.98049.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTACGAGCG
Plate: 17 row: C column: 20
Seq primer: ATTAGTGACATAG.
Location/Qualifiers
1. -513
source
forcan1--"Bov Capuco"

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/db_xref="taxon:9913"
/clone.lib="PARC 5BOV"
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/lab.host="DH10B"
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT          126  a   150  c   130  g   107  t
ORIGIN

Query Match          9.6%;  Score 50.2;  DB 10;  Length 513;
Best Local Similarity 81.7%;  Pred. No. 0.18;
Matches 58;  Conservative 0;  Mismatches 13;  Indels 0;  Gaps 0;
Matches 58;  Conservative 0;  Mismatches 13;  Indels 0;  Gaps 0;
QY          25 CTACCAACAGAGCTCCCTTTAAAGCTTAGGAAAGTCCAGGGATGCC 84
Db          443 CTGCCCAAGAGCPTCTGCTCAAGTGCCTAGGAAAGTCCAGGTGATGCC 502
QY          85 GCAGCGCTCCA 95
Db          503 GCAGGAGCTGCA 513

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Search completed: May 8, 2002, 09:29:36
Job time: 5849 sec

RESULT 15
 BE480590 LOCUS BE480590 DEFINITION 165716 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
 ACCESSION BE480590
 VERSION BE480590.1 GI:96600123
 KEYWORDS EST.
 SOURCE cow.

98-680-514-4-copy_526_L0411.123

Wed May 8 14:05:50 2002

RESULT	1	525 bp	DNA	linear	PAT 29-SEP-1997
LOCUS	E02574	525 bp	DNA	encoding	stimulating factor derivative.
DEFINITION	E02574	525 bp	DNA	human	colon
ACCESSION	E02574	525 bp	DNA	stimulating	factor derivative.
VERSION	1	525 bp	DNA	synthetic	construct.
KEYWORDS	JP 1990227075-A2/	525 bp	DNA	synthetic	construct.
SOURCE	JP 1990227075-A2/	525 bp	DNA	synthetic	construct.
ORGANISM	JP 1990227075-A2/	525 bp	DNA	synthetic	construct.
REFERENCE	1 (bases 1 to 525)	525 bp	DNA	YASUMURA, S.,	
AUTHORS	1 (bases 1 to 525)	525 bp	DNA	Sato, M. and Itoh, S.	
TITLE	1 (bases 1 to 525)	525 bp	DNA		
JOURNAL	1 (bases 1 to 525)	525 bp	DNA		
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PC	JP 1990227075-A2/	525 bp	DNA		
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PF	JP 1988245705	525 bp	DNA		
PR	JP 1988245705	525 bp	DNA		
PI	JP 1988245705	525 bp	DNA		
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KATSUTOSHI	JP 1988245705	525 bp	DNA		
NISHI	JP 1988245705	525 bp	DNA		
TATSUYA	JP 1988245705	525 bp	DNA		
YASUMURA	JP 1988245705	525 bp	DNA		
SHIGETOSHI	JP 1988245705	525 bp	DNA		

SUMMARIES				Description	
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and is derived	8

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QY	445	GGGGGGGGCTTACTTGGCTCCATTCTGAGACTTCCTGGAGGTGTA	504	QY	505	CGCCACCTTGGCCAGGCC	522
Db	445	GGGGGGGGCTTACTTGGCTCCATTCTGAGACTTCCTGGAGGTGTA	504	Db	505	CGCCACCTTGGCCAGGCC	522
QY	505	CGCACCTTGCCAGGCC	522	QY	505	CGCACCTTGCCAGGCC	522
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DEFINITION	Sequence 1 from patent US 5994518.			DEFINITION	CDNA encoding hG-CSF	form human	peripheral macrophage.
ACCESSION	AR091731			ACCESSION	E01731		
VERSION	AR091731.1			VERSION	E01731.1	GI:2169984	
KEYWORDS				KEYWORDS			
SOURCE	Unknown.			SOURCE	Homo sapiens.		
ORGANISM	Unclassified.			ORGANISM	Homo sapiens.		
REFERENCE	1 (bases 1 to 525)			REFERENCE	1 (bases 1 to 525)		
AUTHORS	Kuga,T., Miyaii,H., Sato,M., Okabe,M., Morimoto,M., Itoh,S.,			AUTHORS	Kuga,T., Komatsu,Y., Miyaii,H., Sato,M., Okabe,M., Morimoto,M., Itoh,S., Yamazaki,M., Yokoo,Y. and Yamaguchi,K.		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			TITLE	NOVEL POLYPEPTIDE		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			JOURNAL	PATENT: JP 1988267292-A 1 04-NOV-1988;		
FEATURES	Location/Qualifiers			COMMENT	OS Human		
source	1..525			COMMENT	PN JP 1988267292-A/1		
BASE COUNT	85 a 192 c 151 g 97 t			COMMENT	PD 04-NOV-1988		
ORIGIN				COMMENT	PD 23-DIC-1987		
Query Match	93.3%	Score 486.8; DB 6; Length 525;		COMMENT	PR 23-DEC-1986		
Best Local Matches	98.6%; Pred. No. 1.4e-80;			COMMENT	PR 306759		
LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	PI KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO YOSHITARU, OKABE MASAMI, MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHITARU, YAMAGUCHI KAZUO		
DEFINITION				COMMENT	PC C12P21/02, C07K13/00, C12N1/20, C12N15/00//A61K37/02, A61K37/02, A61K37/02, C12P21/02, C12R1:91;		
VERSION	AR0918485			COMMENT	PC (C12P21/02, C12R1:91); CC strandedness: Double; CC topology: Linear; CC hypothetical: No; CC *source: cell_line-Peripheral macrophage; CC Key Location/Qualifiers		
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ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
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ORGANISM	Unclassified.			COMMENT	FT 1..525		
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AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
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SOURCE	Unknown.			COMMENT	FT 1..525		
ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
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source	1..525			COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
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ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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Best Local Matches	98.6%; Pred. No. 1.4e-80;			COMMENT	FT 1..525		
LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
KEYWORDS				COMMENT	FT 1..525		
SOURCE	Unknown.			COMMENT	FT 1..525		
ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
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ORIGIN				COMMENT	FT 1..525		
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Best Local Matches	98.6%; Pred. No. 1.4e-80;			COMMENT	FT 1..525		
LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
KEYWORDS				COMMENT	FT 1..525		
SOURCE	Unknown.			COMMENT	FT 1..525		
ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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ORIGIN				COMMENT	FT 1..525		
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LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
KEYWORDS				COMMENT	FT 1..525		
SOURCE	Unknown.			COMMENT	FT 1..525		
ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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BASE COUNT	85 a 192 c 151 g 97 t			COMMENT	FT 1..525		
ORIGIN				COMMENT	FT 1..525		
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Best Local Matches	98.6%; Pred. No. 1.4e-80;			COMMENT	FT 1..525		
LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	FT 1..525		
DEFINITION				COMMENT	FT 1..525		
VERSION	AR0918485			COMMENT	FT 1..525		
KEYWORDS				COMMENT	FT 1..525		
SOURCE	Unknown.			COMMENT	FT 1..525		
ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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Query Match	93.3%; Score 486.8; DB 6; Length 525;			COMMENT	FT 1..525		
Best Local Matches	98.6%; Pred. No. 1.4e-80;			COMMENT	FT 1..525		
LOCUS	491; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		COMMENT	FT 1..525		
DEFINITION				COMMENT	FT 1..525		
VERSION	AR0918485			COMMENT	FT 1..525		
KEYWORDS				COMMENT	FT 1..525		
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ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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VERSION	AR0918485			COMMENT	FT 1..525		
KEYWORDS				COMMENT	FT 1..525		
SOURCE	Unknown.			COMMENT	FT 1..525		
ORGANISM	Unclassified.			COMMENT	FT 1..525		
REFERENCE	1 (bases 1 to 525)			COMMENT	FT 1..525		
AUTHORS	Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.			COMMENT	FT 1..525		
TITLE	Method of producing a polypeptide having human granulocyte colony stimulating factor activity			COMMENT	FT 1..525		
JOURNAL	Patent: US 5994518-A 1 30-NOV-1999;			COMMENT	FT 1..525		
FEATURES	Location/Qualifiers			COMMENT	FT 1..525		
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BASE COUNT	85 a 192 c 151 g 97 t			COMMENT	FT 1..525		
ORIGIN				COMMENT	FT 1..525		
Query Match	93.3%; Score 486.8; DB 6; Length 525;			COMMENT	FT 1..525		
Best Local Matches	98.6%; Pred. No. 1.4e-80;			COMMENT	FT 1..525		
LOCUS</							

QY	325	GAACGTGCGCCGACTTGTCCACCAACCATCTGGCAGAGATGGAGAACTGGGATGGCCCT	384	QY	85	GCAGGCCTCCAGGAGAACCTGTGCAACCTAACGCTGTGGCACCCGAGGACTGGCTGGT	144
Db	325	GAACGTGCGCCGACTTGTCCACCAACCATCTGGCAGAGATGGAGAACTGGGATGGCCCT	384	Db	85	GCAGGCCTCCAGGAGAACCTGTGCAACCTAACGCTGTGGCACCCGAGGACTGGCTGGT	144
QY	385	GCCCCCTGGAGCCACCCAGGTGCCATGGCGGCCCTGGCGCTGTGCTTCCACGCCGGCA	444	QY	145	CtGCTCGGACACACTCTGGCATTCGGCTATCCCCTGGCTCCCTAGACGCTGCCAGGGCC	204
Db	385	GCCCCCTGGAGCCACCCAGGTGCCATGGCGGCCCTGGCGCTGTGCTTCCACGCCGGCA	444	Db	145	CtGCTCGGACACACTCTGGCATTCGGCTATCCCCTGGCTCCCTAGACGCTGCCAGGGCC	204
QY	445	GAAGGGGGTCTCATGTTGCTCCATCTGAGACGCTCTGGAGGTGTCGTACCGCTTCTA	504	QY	205	CTGAGCTGGCAGGCTGCTGTGAGCCAACTCCATGGCAGCTTCTAACAGGGCTC	264
Db	445	GAAGGGGGTCTCATGTTGCTCCATCTGAGACGCTCTGGAGGTGTCGTACCGCTTCTA	504	Db	205	CTGAGCTGGCAGGCTGCTGTGAGCCAACTCCATGGCAGCTTCTAACAGGGCTC	264
QY	505	GCCCCACCTTGGCCAGGCC	522	QY	265	CTGGAGGCCCTGGAAAGGGATCTGCCGAGTTGCCACCTTGGCACACTGGCTGGCT	324
Db	505	GCCCCACCTTGGCCAGGCC	522	Db	265	CTGAGGCCCTGGAAAGGGATCTGCCACCTTGGCACACTGGCTGGCTGGCT	324
RESULT	7			QY	325	GACGTCGCCGACTTTGCCACCATCTGGAGGATGGAAACTGGGAATGGCCCT	384
LOCUS	E02573		525 bp	RNA	linear	PAT 29-SEP-1997	
DEFINITION		DNA encoding human colony-stimulating factor(hG-CSF).		QY	385	GCCTCTGCAAGCCACCCAGGGTGCATGGCCTTCGCCTCTGGCTCCAGGCGGCA	444
ACCESSION	E02573			Db	385	GCCTCTGCAAGCCACCCAGGGTGCATGGCCTTCGCCTCTGGCTCCAGGCGGCA	444
VERSION	E02573.1	GI:2170803		QY	445	GGAGGGGTCCTAGTGCCTCCATCTGGAGAGCTTCCTGGAGGTGTCGTACCGGTCTA	504
REVISION				Db	445	GGAGGGGTCCTAGTGCCTCCATCTGGAGAGCTTCCTGGAGGTGTCGTACCGGTCTA	504
ORGANISM	Homo sapiens			QY	505	CGCCACCTTGCCAGGCC	522
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 525)			Db	505	CGCCACCTTGCCAGGCC	522
REFERENCE	Sasaki,K., Nishi,T., Yasumura,S., Sato,M. and Itou,S.			RESULT	8		
AUTHORS	NEW POLYPEPTIDE			E07164			
TITLE	JP 1990227075-A 1 10-SEP-1990;			LOCUS	E07164		
JOURNAL	KYOWA HAKKO KOGYO CO LTD			DEFINITION	CDNA encoding human G-CSF.		
COMMENT	OS Homo sapiens (human)			ACCESSION	E07164		
	PN JP 1990227075-A/1			VERSION	E07164.1	GI:2175311	
PD	10-SEP-1990			KEYWORDS	1 (bases 1 to 525)		
PF	28-SEP-1989	JP 1989253097		ORGANISM	Homo sapiens		
PR	29-SEP-1988	JP 88P 245705		DEFINITION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
PI	SASAKI KATSUTOSHI, NISHI TATSUYA, YASUMURA SHIGEYOSHI, PI			ACCESSION	E07164		
PI	SATO MORIYUKI, PI			VERSION	E07164.1	GI:2175311	
PI	ITOU SEIGA			KEYWORDS	1 (bases 1 to 525)		
PC	C12N9/72,C07K13/00,C07K15/14,C12N1/21,C12N9/64, PC			ORGANISM	1 (bases 1 to 525)		
PC	C12N15/58,C12N15/70,C12N15/85,C12P21/02,C12P21/02, (C12N1/21, C12R1:19), (C12P21/02,C12R1:19), (C12P21/02,C12R1:91);			REFERENCE	Kuga,T., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M., Itou,S., Yamazaki,M., Yoko,Y. and Yamaguchi,K.		
CC	strandness: Double;			AUTHORS	Itou,S., Yamazaki,M., Yoko,Y. and Yamaguchi,K.		
CC	topology: Linear;			SOURCE	NEW POLYPEPTIDE		
CC	hypothetical: No;			TITLE	JP 199022994-A 1 05-APR-1994;		
CC	anti-sense: No;			JOURNAL	KYOWA HAKKO KOGYO CO LTD		
CC	*source: cell_type=lymphoblast Lukii;			COMMENT	OS Homo sapiens (human)		
CC	*source: clone=pcSF1-2;			PD	05-APR-1994		
PH	mat_peptide	1. 522	/product="human colony-stimulating FT	PD	05-APR-1994		
FT			factor(hG-CSF),	PF	23-DEC-1987	JP 1992214376	
			/organism="Homo sapiens"	PR	23-DEC-1986	JP 86P 306799	
			/db_xref="taxon:9606"	PI	KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI		
FEATURES	source	1. 525		PI	MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOZO, YOKOO YOSHITARU, PI		
BASE COUNT	491			PI	YAMAGUCHI KAZUO, C07K13/00,A61K37/02,C12N1/21,C12N15/27,C12P21/02, (C12N1/21, C12P21/19), (C12P21/02,C12R1:19);		
ORIGIN		85 a	192 c	PC	(C12P21/02,C12R1:19);		
		151 g	97 t	PC	C07K13/00,A61K37/02,C12N1/21,C12N15/27,C12P21/02, (C12N1/21, C12P21/19);		
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				FT	/clone="PCSF1-2,"		
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				FT	/cell-type=macrophage;		
				FT	/clone="PCSF1-2,"		

FEATURES	FT CDS	1. .525 /product= 'human G-CSF'.
source	FT	Location/Qualifiers
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BASE COUNT	85 a	/db_xref="Taxon_9606"
ORIGIN		
Query	Match 93.3%; Score 486.8; DB 6; Length 525;	
Best Local Similarity	98.6%; Prod. No. 1.4e-80;	
Matches	491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Db	25 CTGCCCCAGAGTCCCTTAAAGCTTAGAGCAAGTGGAAAGATCCAGGGATGGC 84	FEATURES
Db	25 CTGCCCCAGAGTCCCTGCTCAGTGGTAGCAAGTAGCAAGTGGAAAGATGGC 84	source
Qy	85 GCAGCGCTCAGAGAAGCTGTTGCCCCACCCACAACCTGTTGCCCCACCCGAGAGCTGGCT 144	source
Db	85 GCAGCGCTCAGAGAAGCTGTTGCCCCACCCACAACCTGTTGCCCCACCCGAGAGCTGGCT 144	BASE COUNT
Qy	145 CTGCTGGGACACTCTCGGGCATCCCTGGCTTCCCTGAGCAGTGGCCAGGCC 204	ORIGIN
Db	145 CTGCTGGGACACTCTCGGGCATCCCTGGCTTCCCTGAGCAGTGGCCAGGCC 204	Query Match 93.3%; Score 486.8; DB 6; Length 525;
Qy	205 CTGAGCTGGAGCTGCTTGGGCCAACTCCTAGGGCCCTTTCCTCTACAGGGCTC 264	Best Local Similarity 98.6%; Prod. No. 1.4e-80;
Db	205 CTGAGCTGGAGCTGCTTGGGCCAACTCCTAGGGCCCTTTCCTCTACAGGGCTC 264	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy	265 CTGAGGGCCCTGAAAGGGATCTTGGGTTCCACCTGGACACACTGGAGCTG 324	mat_Peptide
Db	265 CTGAGGGCCCTGAAAGGGATCTTGGGTTCCACCTGGACACACTGGAGCTG 324	FT
Qy	325 GAGGTGGCCGACTTTGCACCACTCTGGAGCACATGGGAAGACTGGGAATGGCCCT 384	Location/Qualifiers
Db	325 GAGGTGGCCGACTTTGCACCACTCTGGAGCACATGGGAAGACTGGGAATGGCCCT 384	1. .525 /organism="Homo sapiens"
Qy	385 GCGCTGAGGCCAACCCAGGGCATGGGCCATGGCCCTTGCCCTTGCCATTGGCAAGGGCA 444	1. .525 /product="G-CSF".
Db	385 GCGCTGAGGCCAACCCAGGGCATGGGCCATGGCCCTTGCCATTGGCAAGGGCA 444	/cell_type="peripheral blood macrophage" FT
Qy	445 GGAGGGGNCCTAGTGGCTCCATCTGGAGACCTCTGGAGGTGCTGTAACGGCTTA 504	mat_Peptide
Db	445 GGAGGGGNCCTAGTGGCTCCATCTGGAGACCTCTGGAGGTGCTGTAACGGCTTA 504	FT
Qy	505 CGCACCTTGGCCAGGCC 522	Location/Qualifiers
Db	505 CGCACCTTGGCCAGGCC 522	1. .525 /organism="Homo sapiens"
RESULT	9	1. .525 /product="G-CSF".
E15131	E15131 525 bp DNA linear	PAT 28-JUL-1999
LOCUS		
DEFINITION	Human mRNA for granulocyte-colony stimulating factor.	
ACCESSION	E15131	
VERSION	E15131.1 GI:5709814	
KEYWORDS	JP 1998052281-A/1	
SOURCE	Homo sapiens	
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 525)	
AUTHORS	Itou,S., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M.,	RESULT 10
TITLE	NEW POLYPEPTIDE	I71150
JOURNAL	Patent: JP 1998052281-A 1 24-FEB-1998;	LOCUS 171150
COMMENT	KYOWA HAKKO Kogyo CO LTD	DEFINITION Sequence 1 from patent US 56681720.
	OS Homo sapiens (human)	ACCESSION I71150
	PN JP 1998052281-A/1	VERSION I71150.1 GI:3007285
	PD 24-FEB-1998	KEYWORDS Unknown.
	PF 23-DEC-1987 JP 1997114630	SOURCE Unknown.
	PR 23-DEC-1986 JP 86P 306799	ORGANISM Unknown.

REFERENCE	Unclassified.	source	1. .525
AUTHORS	(bases 1 to 525) Kuga, T., Miyaji, H., Sato, M., Okabe, M., Morimoto, M., Itoh, S., Yamasaki, M., Yokoo, Y., Yamaguchi, K., Yoshida, H., and Komatsu, Y.	BASE COUNT	85 a 192 c 151 g 97 t
TITLE	DNA encoding human granulocyte colony stimulating factor plasmids and host cells comprising same, and methods of expressing the encoded polypeptide	ORIGIN	0;
JOURNAL	Patent: US 5618720-A 1 28-OCT-1997;		
FEATURES	Location/Qualifiers		
source	1. .525 /organism="unknown"		
BASE COUNT	85 a 192 c 151 g 97 t		
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Best Local Similarity	98.6%; Pred. No. 1.4e-80;		
Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
Qy 25 CTACACAGCTCTTAAAGCTTAGAGAAGTAGGGAGATCAGGGCATGCC 84	Query Match	93.3%; Score 486.8; DB 6; Length 525;	
Db 25 CTGCCCCAGAACCTCTGCTTCAGTGGCTTGGCCACCTACAGCTGTGCCAGGGATGCC 84	Best Local Similarity	98.6%; Pred. No. 1.4e-80;	
Qy 85 GCAGGGCTCCAGGAAGCTGTGGCTTGGCCACCTACAGCTGTGCCAGGGCTG 144	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
Db 85 GCAGGCCTCCAGGAAGCTGTGGCTTGGCCACCTACAGCTGTGCCAGGGCTG 144	Query Match	93.3%; Score 486.8; DB 6; Length 525;	
Qy 145 CTGCTTCGGGACACTCTGGCATCCCTGGCTGGCCAGCTGCCCCAGGCC 204	Best Local Similarity	98.6%; Pred. No. 1.4e-80;	
Db 145 CTGCTTCGGGACACTCTGGCATCCCTGGCTGGCCAGCTGCCCCAGGCC 204	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
Qy 205 CTGAGGCGCTGGAGGGATCTCCCGAGTTGGCTCCACCTTGACACACTGCACTG 324	Query Match	93.3%; Score 486.8; DB 6; Length 525;	
Db 205 CTGAGGCGCTGGAGGGATCTCCCGAGTTGGCTCCACCTTGACACACTGCACTG 324	Best Local Similarity	98.6%; Pred. No. 1.4e-80;	
Qy 265 CTGAGGCGACTTGGCACCACCATCTGGAGATGAAGAACCTGGGAATGGCCCT 384	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
Db 265 CTGAGGCGACTTGGCACCACCATCTGGAGATGAAGAACCTGGGAATGGCCCT 384	Query Match	93.3%; Score 486.8; DB 6; Length 525;	
Qy 325 GACGTGGGACTTGGCACCACCATCTGGAGATGAAGAACCTGGGAATGGCCCT 384	Best Local Similarity	98.6%; Pred. No. 1.4e-80;	
Db 325 GACGTGGGACTTGGCACCACCATCTGGAGATGAAGAACCTGGGAATGGCCCT 384	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
Qy 385 GACGTGGGACTTGGCACCACCATCTGGAGATGAAGAACCTGGGAATGGCCCT 384	Query Match	93.3%; Score 486.8; DB 6; Length 525;	
Db 385 GACGTGGGACTTGGCACCACCATCTGGAGATGAAGAACCTGGGAATGGCCCT 384	Best Local Similarity	98.6%; Pred. No. 1.4e-80;	
Qy 445 GGAGGGGTTCTAGTTGGCTTCCATCTGGAGCTTCCCTGGAGGTGCTGTTCTG 504	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
Db 445 GGAGGGGTTCTAGTTGGCTTCCATCTGGAGCTTCCCTGGAGGTGCTGTTCTG 504	Query Match	93.3%; Score 486.8; DB 6; Length 525;	
Qy 505 CGCCACCTGGCCACCCACCCAGGTGCATGGCGCTTCGCTTCCAGGCCGCC 522	Best Local Similarity	98.6%; Pred. No. 1.4e-80;	
Db 505 CGCCACCTGGCCACCCAGGTGCATGGCGCTTCGCTTCCAGGCCGCC 522	Matches 491; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
RESULT 1.1			
183709	183709	525 bp	DNA
LOCUS	Sequence 1 from patent US 5714581.	linear	PAT 10-AUG-1998
DEFINITION			
ACCESSION	183709		
VERSION	183709.1		
KEYWORDS	i.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 525)		
AUTHORS	Yamasaki, M., Yokoo, Y., Yamaguchi, K., Yoshida, H., and Komatsu, Y.		
TITLE	Polypeptide derivatives of human granulocyte colony stimulating factor		
JOURNAL	Patent: US 5714581-A 1 03-FEB-1998;		
FEATURES	Location/Qualifiers		

[1]	RN	07-OCT-1997 (Rel. 52, Created)
	DE	DT 02-SEP-2000 (Rel. 65, Last updated, version 2)
	XX	CDNA encoding hG-CSF.
	KW	JP 1995149798-A/1.
	XX	Homo sapiens (human)
	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
	OC	
	XX	
	RP	[1] Kuga, T., Komatsu, Y., Miyaji, H., Sato, M., Okabe, M., Morimoto, M., Itoh, S., Yamasaki, M., Yokoo, Y., Yamaguchi, K.; "NEW POLYPEPTIDE"; Patent number JP1995149798-A/1, 13-JUN-1995. KYOWA HAKKO KOGYO CO LTD.
	RA	
	RA	
	RA	
	RL	

XX	OS	Homo sapiens (Human)	DEFINITION	Human granulocyte colony stimulating factor mRNA, complete cds.
CC	PN	JP 199519798 A/1	ACCESSION	M17706
CC	PD	13-JUN-1995	VERSION	M17706.1 GI:183040
CC	PF	08-AUG-1994 JP 1994185787	KEYWORDS	granulocyte colony stimulating factor.
CC	PR	23-DEC-1986 JP 86P 306799	SOURCE	Human MIA PACA 2 cell line, cDNA to mRNA, (library of Kawasaki et al.), clone pP12.
CC	PI	OKABE MASAMI,	ORGANISM	Homo sapiens
CC	PI	MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTO, YOKOO YOSHIEHARU,	MAMMALIA: Eutheria; Chordata; Vertebrata; Catarrhini; Hominidae; Homo.	
CC	PI	YAMAGUCHI KAZUO	REFERENCE	1 (bases 1 to 660)
CC	PC	C07K14/535, C12N1/21, C12N15/09, C12P21/02//A61K38/00, (C12N1/21	AUTHORS	Devlin, J.J., Devlin, P.E., Myambo, K., Lilly, M.B., Rado, T.A. and Warren, M.K.
CC	PC	C12R1.19/	TITLE	Expression of granulocyte colony-stimulating factor by human cell lines
CC	PC	(C12P21/02, C12R1.19);	JOURNAL	J. Leukoc. Biol. 41, 302-306 (1987)
CC	CC	strandedness: Single;	MEDLINE	87196936
CC	CC	topology: Linear;	FEATURES	Location/Qualifiers
CC	FH	Key	source	1. .525 /organism="Homo sapiens"
CC	FH		source	1. .525 /organism="Homo sapiens"
XX			KEY	Location/Qualifiers
FH	source			1. .525 /db_xref="taxon:9606"
FT	FT			/organism="Homo sapiens"
FT	FT			
XX				
SO	Sequence	525 BP; 85 A; 192 C; 151 G; 97 T; 0 other;		
Query	Match	93.3%	Score	486.8; DB 23; Length 525;
Best	Local Similarity	98.6%	Pred.	No. 1.4e-80;
Matches	491; Conservative	0; Mismatches	7; Indels	0; Gaps
Db	25	CTAACACAGCTCCCTTAAAGCTTAGCAGCTGAGAAGATGCCAGGGATGGC 84	mat_peptide	mat
Db	25	CTGCCCCAGAGCTCCCTCAAGTGTCTTAAAGCTTAGCAGCTGAGAAGATGCCAGGGATGGC 84	BASE COUNT	116 a
Qy	85	GCAGCGCTCAGGAGAAAGCTGTTGACCTACAAAGCTGTTGCCACCCGAGGAGCTGGT 144	ORIGIN	243 c
Db	85	GCAGCGCTCAGGAGAAAGCTGTTGACCTACAAAGCTGTTGCCACCCGAGGAGCTGGT 144		188 g
Qy	145	CTGCTGGGACACTCTGGGATCTCCGGATCCTGGGCTCCCTGAGCAGCTGCCAGGGCC 204	Query Match	93.38;
Db	145	CTGCTGGGACACTCTGGGATCTCCGGATCCTGGGCTCCCTGAGCAGCTGCCAGGGCC 204	Best Local Similarity	98.68;
Qy	145	CTGCTGGGACACTCTGGGATCTCCGGATCCTGGGCTCCCTGAGCAGCTGCCAGGGCC 204	Pred.	No. 1.4e-80;
Db	145	CTGCTGGGACACTCTGGGATCTCCGGATCCTGGGCTCCCTGAGCAGCTGCCAGGGCC 204	Mismatches	7;
Qy	205	CTGCACTGGCAGGCTGCTTGGCCAACTCACTAGGCCCTTCTCTCAGCAGGGCTC 264.	Indels	0;
Db	205	CTGCACTGGCAGGCTGCTTGGCCAACTCACTAGGCCCTTCTCTCAGCAGGGCTC 264	Gaps	0;
Qy	265	CTGAGGGCCCTGAAAGGATCTCCCGAGTGGGCCAACCTGGACACCTGGACAGCTG 324	mat_peptide	mat
Db	265	CTGAGGGCCCTGAAAGGATCTCCCGAGTGGGCCAACCTGGACACCTGGACAGCTG 324	BASE COUNT	116 a
Qy	325	GAGTCGGGACCTTGGCACCACATCTGGAGCAGATGGAGAACCTGGGAATGGCCCT 384	ORIGIN	243 c
Db	325	GAGTCGGGACCTTGGCACCACATCTGGAGCAGATGGAGAACCTGGGAATGGCCCT 384		188 g
Qy	385	GCTCTGGGACCCACCCAGGCTCCATGCCGCTTGGGAGGCTTCTGAGGAGCTCTA 444	Query Match	93.38;
Db	385	GCTCTGGGACCCACCCAGGCTCCATGCCGCTTGGGAGGCTTCTGAGGAGCTCTA 444	Best Local Similarity	98.68;
Qy	445	GGAGGGCTCTAGTTGCTCCATCTGGAGGCTTCTGAGGAGCTTCTGAGGAGCTCTA 504	Pred.	No. 1.4e-80;
Db	445	GGAGGGCTCTAGTTGCTCCATCTGGAGGCTTCTGAGGAGCTTCTGAGGAGCTCTA 504	Mismatches	7;
Qy	505	CGCACCTGGCCAGGCC 522	Indels	0;
Db	505	CGCACCTGGCCAGGCC 522	Gaps	0;
RESULT	13			
HUNGCSF				
LOCUS	HUMGCSF			
		660 bp	mRNA	linear
			PRI	27-APR-1993

Qy	25	CTACACAGAGCTTAAAGCTTAGAACAGTGAAGGAAGATCCAGGGCATGGC	84
Db	145	CTGCCCAAGCTCCTGCTCAGTGTCTAGCAAGTGAAGATCCAGGGATGGC	204
Qy	85	GCAGGGCTCAGAGAAAGCTGTGTGCAACCTACAAGCTGTGCAACCCGAGGGCTGGT	144
Db	205	GCAGGGCTCAGAGAAAGCTGTGTGCAACCTACAAGCTGTGCAACCCGAGGGCTGTG	264
Qy	145	CTGCTGGGACACTCTGGGATCCTCTGGCTCCCTGAGZAGCTGCCCAAGGCC	204
Db	265	CTGCTGGGACACTCTGGGATCCTCTGGCTCCCTGAGZAGCTGCCCAAGGCC	324
Qy	205	CTGAGCTGGCAGGGTGGCTGAGCCAACCTCATAGCGGCCCTTTCCTACAGGGCTC	264
Db	325	CTGAGCTGGCAGGGTGGCTGAGCCAACCTCATAGCGGCCCTTTCCTACAGGGCTC	384
Qy	265	CTGAGGGCTGGAAAGGGATCTCCCGAGTTGGTCCCACCTTGGACACACTGCACTG	324
Db	385	CTGAGGGCTGGAGGATCTCCCGAGTTGGTCCCACCTTGGACACACTGCACTG	444
Qy	325	GACCTGGCGGAGACTTGGCACACATGGCAGCATGGAGAACTGGAACTGGAACTGGCA	384
Db	445	GACCTGGCGGAGCTTGGCACACATCTGGCAGCATGGAGAAACTGGAAACTGGAACTGGCA	504
Qy	385	GCCCTGACCCACGGTGCCTATGGCGCTTCCCTCTGGCATGGCGGGCA	444
Db	505	GCCCTGACCCACGGTGCCTATGGCGCTTCCCTCTGGCATGGCGGGCA	564
Qy	445	GGAGGGCTCTAGTTGGCTCCCATCTGGAGAGCTTCTGGAGGTGTGTAACGGTCTA	504
Db	565	GGAGGGCTCTAGTTGGCTCCCATCTGGAGCTTCTGGAGGTGTGTAACGGTCTA	624
Qy	505	CGCACCTGGCCAGGCC	522
Db	625	CGCACCTGGCCAGGCC	642

Search completed: May 8, 2002, 10:02:06
 Job time: 779 sec